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MPsrch\_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu May 6 15:00:47 1999; Maspar time 1644.23 Seconds

Tabular output not generated.  
Title: 1384.282 Million cell updates/sec

Description: >US-09-037-460-1  
(1-1271) from US09037460.seq

N.A. Perfect Score: 1266 Comp:

Sequence: 1 CTGGTCTCCACCGCAARGA.....GTTNCCCNNTCTNAAAGAC 1271  
GAGCAAGGGTGTCGTTCT.....CAANGGANANAGANTTCCTG

Scoring table: TABLE default  
Gap 6

Match STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

emb1-est56  
1:em\_est1\_2:em\_gss1 3:em\_gss2 4:em\_gss3

genbank-est109  
5:gb\_est1\_6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13

10:gb\_est14 11:gb\_est15 12:gb\_est16 13:gb\_est17

14:gb\_est18 15:gb\_est19 16:gb\_est2 17:gb\_est20

18:gb\_est21 19:gb\_est3 20:gb\_est4 21:gb\_est5 22:gb\_est6

23:gb\_est7 24:gb\_est8 25:gb\_est9 26:gb\_gss1 27:gb\_gss2

28:gb\_gss3 29:gb\_gss4

Statistics: Mean 11.873; Variance 3.231; scale 3.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.	
1#	412	32.5	425	21	W46667 zc33e02_r1 Soares sene	0.00e+00	
2	139	11.0	351	24	A0296597 EST112419 Aorta endoth	1.44e-152	
c	3	62	4.9	252	12	AAT754459 97SN1787 Rice Immature	1.37e-44
c	4	56	4.4	252	12	AAT754459 97SN1787 Rice Immature	6.87e-37
c	5	48	3.8	247	12	AAT754458 97SN1784 Rice Immature	5.86e-27
c	6	46	3.6	247	12	AAT754458 97SN1784 Rice Immature	1.51e-24
c	7	35	2.8	2275	11 AF034173 Homo sapiens ntcon2 co	5.24e-12	
c	8	33	2.6	236	11 AAT03386 z290b06_s1 Soares pine	6.83e-10	
c	9	30	2.4	467	29 A0191727 HS_3095_A2_G04_T7 CIT	7.59e-07	
c	10	29	2.3	199	14 AAV26494 TENS116_T. cruzi epim	7.20e-06	
c	11	29	2.3	265	15 A0005619 ov15f08_s1 NCI_CGAP_GC	7.20e-06	
c	12	29	2.3	284	14 AAB90895 T. cruzi epim	7.20e-06	
c	13	29	2.3	369	10 AA642307 ns25b12_s1 NCI_CGAP_GC	7.20e-06	

FEATURES

Source

Contact: Wilson RK  
WashU Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 1322 Std Error: 0.00  
Seq. Primer: mob.REGA+ET  
Unpublished (1995)  
High quality sequence stop: 395.  
Location/Qualifiers  
1. 425  
/organism="Homo sapiens"  
/note="Vector: pT7T3D (Pharmacia) with a modified  
PolyLinker V TYPE: phagemid; Site\_1: Not I; Site\_2: Eco

#### ALIGNMENTS

RESULT  
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LOCUS  
W46667 425 bp mRNA  
DEFINITION zc33e02\_r1 Soares senescent fibroblasts EST  
ACCESSION W46667 11-OCT-1996  
NID 91331295  
KEYWORDS  
ORGANISM Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
SOURCE vertebrates; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Hillier,L., Clark,N., Dubucque,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)



TITLE	Lee, M.C. and Eun, M.Y.
JOURNAL	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
COMMENT	Unpublished (1998)
FEATURES	<p>Contact: Eun M.Y.            Department of Cytogenetics            National Inst. of Agri. Sci. and Tech, RDA            Suwon, Kyunggi-do, Korea            Tel: 82 31 290 001            Fax: 82 31 290 0307            Email: myeun@sun20.asti.re.kr            Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bnhnahm@biobserver.myongji.ac.k            Seq primer: M13 Reverse Primer.            Location/Qualifiers            1. 1..252            /organism="Oryza sativa"            /cultivar="Milyang23"            /note="Vector: PB Bluescript SK(+) ; Site_1: EcoRI; Site_2:            xhoI: Directional CDNA library inserted into Lambda ZAP            vector at 5' end with EcoRI and 3' end with Xba I site."            /db_xref="taxon:4530"            /clone="97SN1187"            /clone_id="Rice Immature Seed Lambda ZAPII cDNA Library"            /tissue_type="Immature Seed"            /dev_stage="5 days after pollination"            /lab_host="E. coli SOLR"            5 a 21 c 12 g 35 t 179 others         </p>
BASE COUNT	6
ORIGIN	
source	<p>Query Match 4.9%; Score 62; DB 12; Length 252;            Best Local Similarity 11.3%; Pred. No. 1.37e-44;            Matches 23; Conservative 107; Mismatches 71; Indels 2; Gaps 2</p> <p>Db 30 VWWCVASHGNMYSVHNCVTRGTHDCKAVNNWSTMTWGTNWBNVSGDWHYBNTKYDV 89            Cp 1102 AAACCAVAAATTAATTCTAGAGAAGCTACCTACCAAGGAAGGGCTAAATTTATTC 1043            Db 90 GNHTRSRMRVBRTRMAYHDYTNCCBYNNNDYHMWHBMYBTTGCMCTMMWBHYNTKC 149            Cp 1042 CACTCCACCCCCCTCCCATCTCTCGTCUTAAAGCTTCAATTCCAACTATCCAACT 983            Db 150 TASGWHSTNVDYKSSTNT-WGVTBSDKSMHGTYWCBBVKVHTKVSSTRATRSYTVRK 208            Cp 982 AATGTAATCAAAGTCAAAAGAACATAATTGACTCACIGCGTCTTCAGCTTGCCCT AGC 924            Db 209 YCVMWWKKVVKVVKYHV/BBGCHB 231            Cp 923 TCCCTCTTTGGTGTGACCTGTCTC 901</p>
RESULT	4
LOCUS	AA754459
DEFINITION	97SN11787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa mRNA
ACCESSION	AA754459
NID	92801165
KEYWORDS	EST.
SOURCE	rice.
ORGANISM	Oryza sativa
REFERENCE	Eukaryote; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida Poales; Poaceae; Oryza.
AUTHORS	1 (bases 1 to 252) Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P., Lee, M.C. and Eun, M.Y.
TITLE	Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL	Unpublished (1998)
COMMENT	Contact: Eun M.Y. Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA

FEATURES	SOURCE	Location/Qualifiers
1. .247		/organism="Orzyza sativa"
/cultivar="Milyang23"		
/note="Vector: pBluescript SK(+)"; Site_1: EcoRI; Site_2:		
XbaI; Directional cDNA library inserted into lambda ZAPII		
vector at 5' end with EcoRI and 3' end with Xba I site."		
/db_xref="taxon:4530"		
/clone="97SN1784"		
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"		
/tissue_type="Immature Seed"		
/dev_stage="5 days after pollination"		
/lab_host="E. coli SOLR"		
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ORIGIN	7 a	21 g
Query Match	3.68;	Score 46;
Best Local Similarity	11.48;	Length 247;
Matches 26;	Conservative	Pred. No. 1.51e-24;
Matches 26;	Mismatches 87;	Indels 4;
		Gaps 3;
Db	16 CBAWNKHTMMTBWWCYYRRVGTNTNNKGHNGTWTNCSDNAHCRTVBWYARSKY 75	
Cp	697 CTATAATCTAGAAACTCCAAATGTCGTGTTGAACTACGAAATAGAGC 638	
Db	76 GYGTBYSWAVDTNGGTGKTVNVHSWNRSNSVYVWATAYDGHYBHDRAHW 135	
.CP	637 CTTCCTCTCAAAATCACGGGGATCAGGTGATTACCATTCCTC-ATTAACGGGA 579	
Db	136 DDTTRCTNDRGYCNYTASDNGTSATKRVTYDKTDSDCGGGCWRKVYGSSSBYBRGVNVM 195	
Cp	578 GACCGGGCACATCTCT - TCACACTCTTCCTCA - CAATATGCCATCTCCAGAT 522	
Db	196 VRTISMTWDKSTKMBSDMDMSRSRVHYGRMBNKKRGMRSNWTDTKTR 244	
Cp	521 GCCATGTCATGCTCGTGAGAGAAAACAAATCTGTGGAAAGACTGGTTA 473	
RESULT	7	AF034173 2275 bp mRNA
LOCUS		EST
DEFINITION	Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.	
ACCESSION	AF034173	
NID	92707735	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
	Primates; Catarrhini; Homidae; Homo.	
REFERENCE	1-(bases 1 to 2275)	
AUTHORS	Tripodis, N. and Raghousis, J.	
TITLE	Generation of a transcription map in the region immediately	
	centromeric to human HMC across the 6p21.2-6p21.3 chromosomal	
	boundary.	
JOURNAL	unpublished	
REMARKS	2 (bases 1 to 2275)	
AUTHORS	Tripodis, N. and Raghousis, J.	
TITLE	Direct Submission	
JOURNAL	Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,	
	Guy's Hospital, 7th Floor, Guy's Tower, London SE1 9RT, UK	
FEATURES	Location/Qualifiers	
	1. 2275	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="6"	
	/map="6p1.3"	
	/clone="ntcon2 contig"	
	/tissue_type="liver; brain"	
	/dev_stage="fetus"	
	/note="similar to Br140"	
BASE COUNT	438 a	619 c 470 g 599 t
ORIGIN	149 others	
Query Match	2.8%	Score 35;
Best Local Similarity	9.5%	DB 11;
Matches 14;	Conservative	Pred. No. 5.2e-12;
	Mismatches 52;	Indels 2;
		Gaps 2;
Db	1481 YKKWKRKGRKRMGKMYRMMAMCMAACWNNWYKRGMKWCWKYKYYKTST 1540	
Cp	1267 TTNAGANANAGGNARACCGGGCTCATCAGCGCTTGTGATCTC-TCAGNTCA 1209	
Db	1541 YYKWSRWYWWYTYWYWWCWTSMKSASCA-MMRWYMGMSRSRWSYWGNGMSGCGY 1599	
Cp	1208 AAGCTGTTGTTACTCAAATTCATAAAGCTCAACATCTACTCCTCAAGGGTTT 1149	
Db	1600 MTKRYRYSWTGTWTWYMSMTRW 1627	



FEATURES	source	Seq primer: T7; Location/Qualifiers 1..199 /organism="Trypanosoma cruzi" /strain="Cl-Brenner" /note="cDNA library constructed with oligo dT primed epimastigote mRNA and cloned in pT7-318D phagemid with modified polylinker (PHARMACIA)" /db_xref="taxon:5693" /clone="116" /cell_type="T. cruzi epimastigote" /base_count="56 a .46 c 37 g 52 t 8 others ORIGIN
		Query Match Best Local Similarity 2.3%; Score 29; DB 14; Length 199; Matches 45; Conservative 0; Gaps 0; LOCUS AA005619 265 bp mRNA EST 12-JUN-1998 DEFINITION Homo sapiens cDNA clone IMAGE:1637415 3' ACCESION A1005619 KEYWORDS EST. SOURCE human. ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; PRIMATES; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 265) REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. AUTHORS Michael Ehmert-Buck, M.D., Ph.D. TITLE CGNA Library Preparation: M. Bento Soares, Ph.D. JOURNAL Tumor Gene Index COMMENT Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Ehmert-Buck, M.D., Ph.D. CGNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/JLNL at: <a href="http://www-bio.llnl.gov/bbrr/image/image.html">www-bio.llnl.gov/bbrr/image/image.html</a>
		Trace considered overall poor quality Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1..265 /organism="Homo sapiens" /note="vector: pT7-3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - Eco RI adaptor (Pharmacia) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7-3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606"
FEATURES	source	Query Match Best Local Similarity 2.3%; Score 29; DB 15; Length 265; Matches 38; Conservative 0; Gaps 0; LOCUS AA005619 265 bp mRNA EST 12-JUN-1998 DEFINITION Homo sapiens cDNA clone IMAGE:1637415 3' ACCESION A1005619 KEYWORDS EST. SOURCE human. ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; PRIMATES; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 265) REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. AUTHORS Michael Ehmert-Buck, M.D., Ph.D. TITLE CGNA Library Preparation: M. Bento Soares, Ph.D. JOURNAL Tumor Gene Index COMMENT Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Ehmert-Buck, M.D., Ph.D. CGNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/JLNL at: <a href="http://www-bio.llnl.gov/bbrr/image/image.html">www-bio.llnl.gov/bbrr/image/image.html</a>
FEATURES	source	Trace considered overall poor quality Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1..265 /organism="Homo sapiens" /note="vector: pT7-3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - Eco RI adaptor (Pharmacia) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7-3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606"

SOURCE	human.
ORGANISM	Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 369)
AUTHORS	NCI-CCAP Project
TITLE	National Cancer Institute, Cancer Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
FEATURES	Unknown library type Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 328.
source	Location/Qualifiers 1..369
	/organism="Homo sapiens" /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XbaI; /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XbaI; This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 336.
FEATURES	Location/Qualifiers 1..369
source	/organism="Homo sapiens" /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XbaI; mRNA made from human bone marrow stroma cDNA made by oligo-dT priming directionally cloned. Size selected for average insert size >0.5 kb. Library supplied by Dr. Libin Jia (NHGRI)." /db_xref="taxon:9606" /clone="119229" /clone_1ib="Jia bone marrow stroma" /sex="mixed" /tissue_type="bone marrow stroma" /dev_stage="mixed" /lab_host="XU-Blue MRF/SOLR"
BASE COUNT	140 a 69 c 50 g 110 t
ORIGIN	
RESULT	15
LOCUS	AA620322
DEFINITION	ar0690.s1 Soares testis NHT Homo sapiens mRNA clone 1030906 3', 14-OCT-1997
ACCESSION	AA620322
NID	92524261
KEYWORDS	
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 379)
AUTHORS	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE	WashU-NCI Human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 371.
source	Location/Qualifiers 1..379
	/organism="Homo sapiens" /note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACCACTGAACTGGACTGGCAGCGCCATTTTTTTTTT-3'].
FEATURES	
source	
BASE COUNT	119 a 86 c 72 g 92 t
ORIGIN	
RESULT	16
LOCUS	AA620323
DEFINITION	ar0690.s1 Soares testis NHT Homo sapiens mRNA clone 1030906 3', 14-OCT-1997
ACCESSION	AA620323
NID	92524261
KEYWORDS	
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 379)
AUTHORS	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE	WashU-NCI Human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 371.
source	Location/Qualifiers 1..379
	/organism="Homo sapiens" /note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACCACTGAACTGGACTGGCAGCGCCATTTTTTTT-3'].
FEATURES	
source	
BASE COUNT	119 a 86 c 72 g 92 t
ORIGIN	
RESULT	17
LOCUS	AA620324
DEFINITION	ar0690.s1 Soares testis NHT Homo sapiens mRNA clone 1030906 3', 14-OCT-1997
ACCESSION	AA620324
NID	92524261
KEYWORDS	
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 379)
AUTHORS	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE	WashU-NCI Human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 371.
source	Location/Qualifiers 1..379
	/organism="Homo sapiens" /note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACCACTGAACTGGACTGGCAGCGCCATTTTTTTT-3'].
FEATURES	
source	
BASE COUNT	119 a 86 c 72 g 92 t
ORIGIN	
RESULT	18
LOCUS	AA620325
DEFINITION	ar0690.s1 Soares testis NHT Homo sapiens mRNA clone 1030906 3', 14-OCT-1997
ACCESSION	AA620325
NID	92524261
KEYWORDS	
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 379)
AUTHORS	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE	WashU-NCI Human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
FEATURES	This clone is available royalty-free through LInL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 371.
source	Location/Qualifiers 1..379
	/organism="Homo sapiens" /note="Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACCACTGAACTGGACTGGCAGCGCCATTTTTTTT-3'].
FEATURES	
source	
BASE COUNT	119 a 86 c 72 g 92 t
ORIGIN	
RESULT	19
LOCUS	AA620326
DEFINITION	ar0690.s1 Soares testis NHT Homo sapiens mRNA clone 1030906 3', 14-OCT-1997
ACCESSION	AA620326
NID	92524261
KEYWORDS	
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 379)
AUTHORS	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE	WashU-NCI Human EST Project
JOURNAL	Unpublished (1997)
COMMENT	Contact: Wilson RK / Jia L WashU-MGB/NHGRI EST Project Washington University School of Medicine

Thu May 6 16:54:39 1999

US-09-037-460-1.rst

Page 8

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT13 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Patima Bonaldo." /db\_xref="taxon:9606" /clone="1030906" /clone\_lib="Soares testis NHT"

BASE COUNT  
ORIGIN  
143 a 71 c 50 g 115 t

Query Match 2.3%; Score 29; DB 10; Length 379;  
Best Local Similarity 78.7%; Pred. No. 7.20e-06;  
Matches 37; Conservative 1; Mismatches 9; Indels 0; Gaps 0;  
Db 257 TTTGCCCTTGC AAGATCCAAAAAAAGCACAGTAA 303  
Cp 1136 TTTGACTTTCCAACCCC AAAAAAAGCAZYTTAA 1090

Search completed: Thu May 6 16:02:01 1999  
Job time : 3194 secs.